

Fig. 1

Allele Calling for di-nucleotide marker in linkage mapping application Sample Data (2)

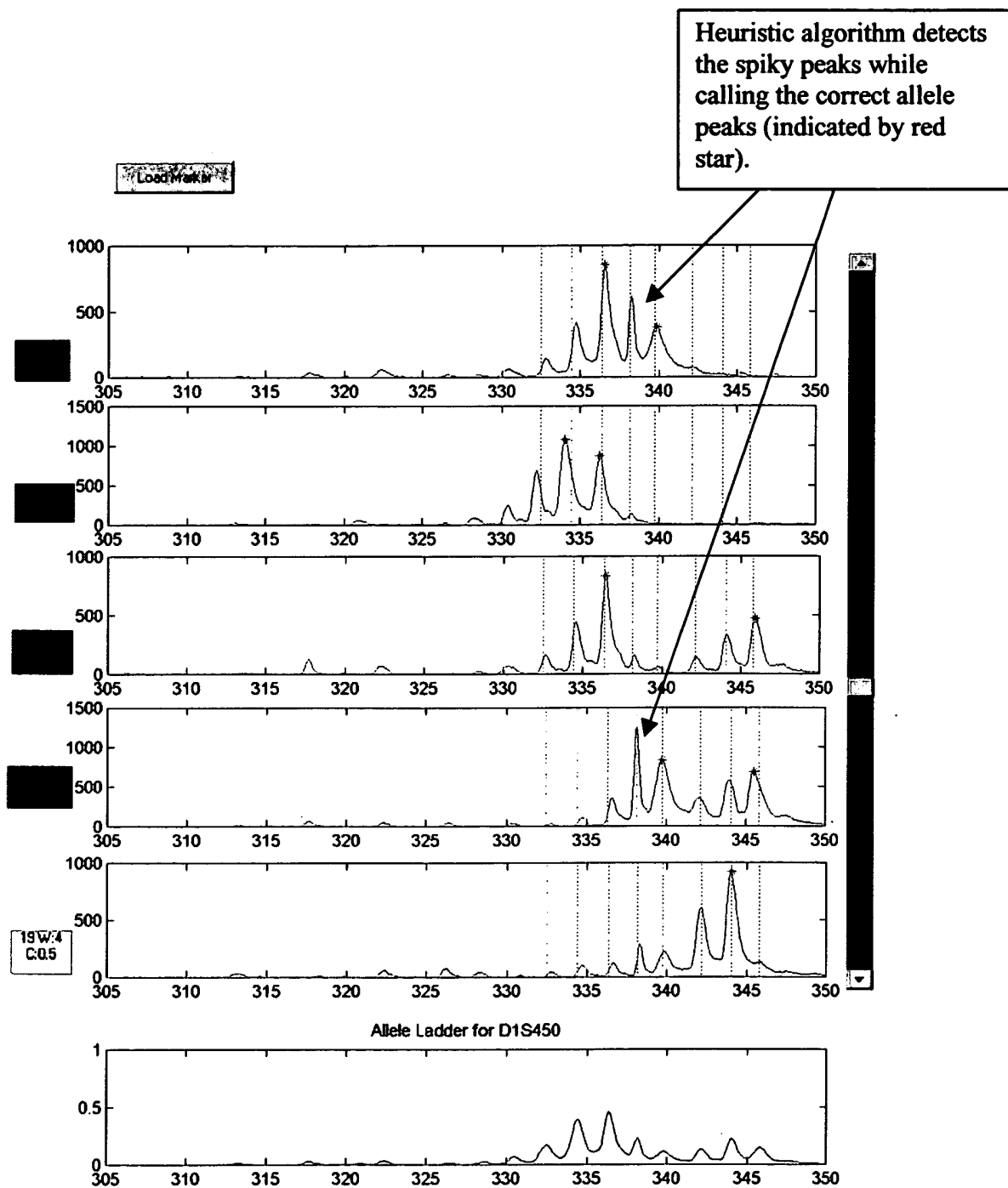


Figure 11

Allele Calling for di-nucleotide marker in linkage mapping application Sample Data (1)

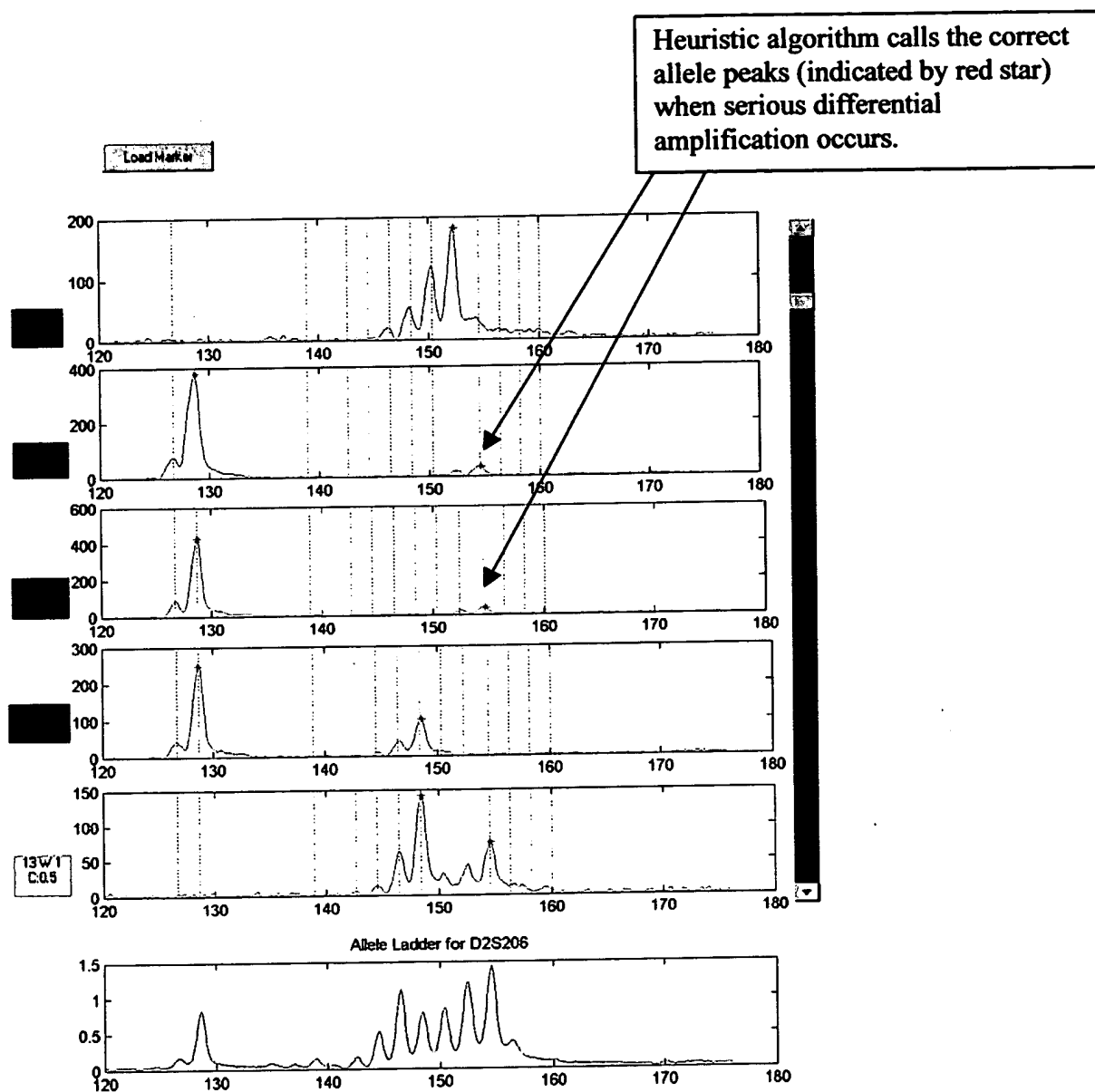


Figure 12

The figure is a line graph representing an X-ray diffraction pattern. The horizontal axis is labeled with '185' at the left end and '235' at the right end. The vertical axis has a label '225' at the top and '0' at the bottom. The plot shows a baseline with low-intensity noise. Two prominent, sharp peaks are visible. The first peak is located at approximately 18.5° on the horizontal axis and reaches a height of about 225 on the vertical axis. The second peak is located at approximately 20.5° on the horizontal axis and reaches a height of about 180 on the vertical axis. Both peaks are marked with a small black dot at their apex.

Figure 13: Standard heterozygous allele signature. Circles denote user annotated allele calls. x-axis is in base pairs. y-axis is in A/D counts (voltage intensity)

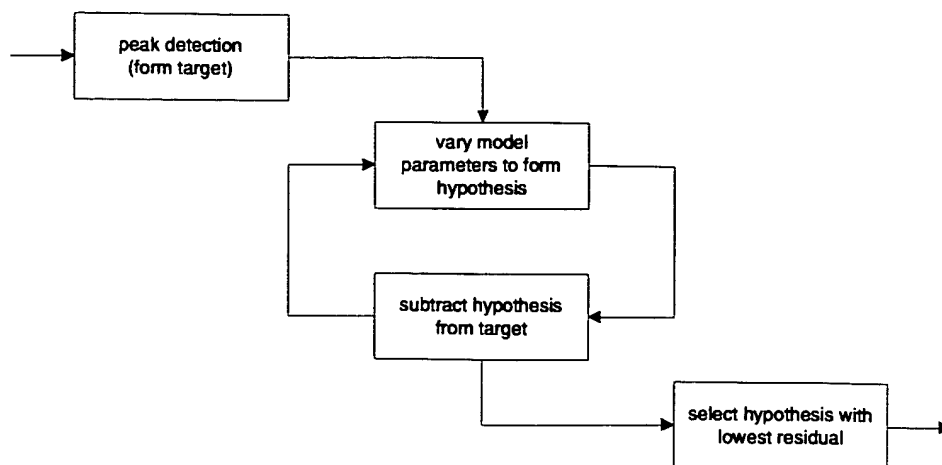


Figure 14: Steps in the allele calling routine. First the signal is simplified via sampling and its peaks are located. This forms the target signal that is to be approximated. The two interconnected boxes indicate the process of varying the parameters and testing how closely the resulting signal matches the sampled version of the original. The set of parameters that yield the closest match contain the allele calls.

The figure is a line graph representing an X-ray diffraction pattern. The vertical axis (y-axis) has labels '0' and '225'. The horizontal axis (x-axis) has labels '180' and '240'. The plot area is divided into six vertical sections by five vertical lines. The third section from the left is labeled 'p1' and contains a sharp, high-intensity peak. The fifth section is labeled 'p2' and contains a smaller, broader peak. Both peaks are marked with a symbol that looks like a phi (ϕ) with an asterisk (*). The baseline of the graph shows low-level noise across all sections, with a label 'p3' in the second section.

Figure 16: Division of heterozygous signal into panels by the Envelope Caller algorithm. The panels are ranked according to signal energy and the three of interest are labeled p1, p2 and p3 with the two panels containing strong allele signatures being shaded in blue. Circles denote user annotated allele calls. x-axis is in base pairs. y-axis is in A/D counts (voltage intensity)